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.a. - n.a. database search, using Smith-Waterman algorithm

Apr 25 18:57:00 1997; MasPar time 1002.71 Seconds 1001.171 Million cell updates/sec

Tabular output not generated

Perfect Score:
N.A. Sequence:
Comp: Description: >US-08-699-716A-1 (1-1566) from US08699716A.seq 1566

1 ATGGGCCATCATCATCATCA......
TACCCGGTAGTAGTAGTAGT......

Scoring table: TABLE Gap 6 default

Dbase 0; Query

887282 segs, 320523884 bases

Post-processing: Minimum n Match g first 0**%**

1:EST1 2:EST2 3:EST3 4:EST4 5:EST5 6:EST6 7:EST8
9:EST9 10:EST10 11:EST11 12:EST12 13:EST13 14:EST14
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33:EST33 34:EST34 35:EST35 36:EST36 37:EST37 38:EST38
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67:EST67 58:EST58 59:EST59 60:EST60 67:EST67 68:EST68
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75:EST75 76:EST76 77:EST77 78:EST78 73:EST79 80:EST80
81:EST81 82:EST82 83:EST83 84:EST48 45:EST49 80:EST80
87:EST87 88:EST88 89:EST89 90:EST90 91:EST91 92:EST99
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Database:

EST-STS-TWO 100:EST100 105:EST110 110:EST110 110:EST110 115:EST115 120:EST120 125:EST125 130:EST130 140:EST140 140:EST140 140:EST140 150:EST150 150:EST150

0 101:EST101 5 106:EST116 0 111:EST116 0 111:EST116 0 121:EST126 5 126:EST126 0 131:EST131 0 131:EST131 5 136:EST136 0 141:EST146 1 141:EST146 1 151:EST151 5 156:EST151 5 156:EST151 5 166:EST156 1 166:EST156 1 166:EST156 1 166:EST156 1 166:EST156 1 166:EST156

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3 104:EST104
3 114:EST1104
6 119:EST1119
6 119:EST1119
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7 134:EST139
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7 149:EST149
8 149:EST149
8 149:EST149
8 159:EST159
7 154:EST159
7 154:EST159
7 154:EST159
7 154:EST159

BEST AVAILABLE COPY

194:STS1 195:STS2 196:STS3 197:STS4 198:STS5 199:STS6 200:STS7 201:STS8 202:STS9 203:STS10 204:STS11 205:STS12 206:weEST 207:gnEST1 208:gnEST2 209:gnEST3 210:gnEST4 211:gnEST5 212:gnEST6 213:gnEST7 214:gnEST8 215:gnEST9 216:gnEST9 217:gnEST11 218:gnEST9 219:gnEST13 220:gnEST14 221:gnEST11 218:gnEST16 223:gnEST1 229:gnEST16 223:gnEST1 229:gnEST16 223:gnEST1 229:gnEST1 240:gnEST1 240:gnEST13 240:gnEST2 240 175:EST175 176:EST176 180:EST180 181:EST181 185:EST185 186:EST186 190:EST190 191:EST191 EST-STS-THREE 8 179:EST179 3 184:EST184 8 189:EST189

Statistics: Variance scale 5.354

score greater than and is derived by a is the number of results predicted by chance to have ater than or equal to the score of the result being partied by analysis of the total score distribution. printed,

Query Match

Description

04 PCU64650
06 G08117
06 G0817
07 G08591
07 G08591
07 G08593
07 G08593
07 G08593
07 G08999
07 G09999
07 G09999
07 G09999
07 G10330 HUMUT6615 HUMUT6615 R76963 R76963 H91490 H91490 G15746 G09469 7 G09478 HUMUT8005B G09256 G10329 G09261 HUMUT7997 HUMUT7997 G09257 R23641 HUMUT1040 Parachartergus colobo
Parachartergus colobo 0 1.04e-13 .04e-13 .04e-13

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DEFINITION
ACCESSION
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AUTHORS
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Primer B: CCAC
STS size: 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cooperative Human Linkage Center Unpublished (1995)
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1 (bases 1 to 451)
Murray, J., Sheffield, V, Weber, J.L.,
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Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta
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human vector=pJCP1 host=E.coli dut+ung+ (DH10B) Marker Selected
genomic DNA prepared from XY individual of French nationality.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g941262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The University of Iowa
Department of Pediatrics,
Tel: (319) 356-3508
Fax: (319) 356-3347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synonyms: ATC1, CHLC.ATC1.T9550 GDB: G00-365-092
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                                                                                                                                          complement(282..301)
92 c 78 g
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169..301
169..188
                                                                                                                                                                                                   Location/Qualifiers
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STS sequence; primer; sequence tagged site.
human vector=pJCPl host=E.coli dut+ung+ (DH
human vector=pJCPl host=E.coli dut+ung+ (DH
human vector=pJCPl host=E.coli dut+ung+ (DH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 231)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified p77 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from 4 multiple sclerosis lesions from one patient was kindly provided by Dr. Kevin G. Becker (NINDS/NIH).
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Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; (
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta
                                                      Homo Sapiens
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Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The WashU-Merck EST Project Unpublished (1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This clone is available royalty-free through LLNL; IMAGE Consortium (info@image.llnl.gov) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence stops: 183 Source: IMAGE Consortium, LLNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Wilson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WashU-Merck EST Project
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/clone="276546"
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AUTHORS
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Matches 3
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U64650;
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                                                                                                     Strassmann J.E., Solis C.R., Barefield K., Queller D.C. "Trinucleotide microsatellite loci in a swarm-founding wasp, Parachartergus colobopterus and their usefulness social wasps";
                                                                                                                                                                                                                                                                                                               19-AUG-1996
19-AUG-1996
  Strassmann J.E.,
Queller D.C.;
                                                                  Mol. Ecol.
[2]
                                                                                                                                                                                                                                                     Parachartergus colobopterus
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Primer B: GGAGCACCAAGTACCATGTC
STS size: 167
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Unpublished (1995)
Synonyms: ATC3C12, CHLC.AT
Contact: Dr. Jeffrey C. Mu
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Department of Pediatrics,
Tel: (319) 356-3508
Fax: (319) 356-3347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  h 2.0%;
Similarity 89.7%;
35; Conservative
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annealing:
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microsatellite Paco3301CAT
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Pred. No. 3.44e-15;
0; Mismatches 4
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repeat_region
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primer_bind :
Sequence 255 BP;
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Parachartergus colobopterus

Parachartergus colobopterus

Eukaryotae; mitochondrial eukaryotes; Metazoa; Arthropoda;

Eracheata; Hexapoda; Insecta; Pterygota; Hymenoptera; Apocrita;

Aculeata; Vespoidea; Vespidae; Polistinae; Parachartergus.

1 (bases 1 to 255)

Strassmann,J.E., Solis,C.R., Barefield,K. and Queller,D.C.

Trinucleotide microsatellite loci in a swarm-founding neotropic;

wasp, Parachartergus colobopterus and their usefulness in other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g1495941
STS.
                                                                                                                                                                                                                                                                                 Submitted (19-JUL-1996) Ecology University, 6100 Main, Houston, Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                   social wasps
Mol. Ecol. 5 (3), 459-461
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Similarity 100.0%;
31; Conservation
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Similarity 100.0%;
31; Conservative
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                                                                                                                                                                  /note="microsatellite"
complement(137..156)
164..208
236..255
a 57 c 90 g
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complement(137..156)
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/clone="Paco3301CAT"
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/clone="Paco3301CAT"
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                                                                                                    Score 31;
Pred. No.
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Pred. No. 3.44e-15;
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                                                                            209
                                                                                                    ; DB 205; I
. 3.44e-15;
matches 0;
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x 77005, USA
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6100 main,
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Paco3301CAT DNA.
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DEFINITION

Parachartergus

colobopterus microsatellite Paco3301CAT DNA

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repeat_region
primer_bind
BASE COUNT 59
ORIGIN
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AUTHORS
TITLE
JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                9938667
STS sequence; primer; sequence tagged site.
human vector-pJCP1 host-E.coli dut+ung+ (DH10B) Marker Selected genomic DNA prepared from XY individual of French nationality.
                Primer A: GCTGGCATGATAAATTGCTT
Primer B: AAATGGCCACTCCCTAAAAC
STS size: 147
PCR Profile:
                                                                                                                     The University of Iowa
Department of Pediatrics,
Tel: (319) 356-3508
Fax: (319) 356-3347
                                                                                                                                                                                                          Cooperative Human Linkage Center Unpublished (1995)
Synonyms: ARC3E01, CHLC.ATC3E01.#T7573
Contact: Dr. Jeffrey C. Murray
                                                                                                                                                                                                                                                                          Tetrapoda; Amniota; Mammalia; Theria
Catarrhini; Hominidae; Homo.
1 (bases 1 to 256)
Murray, J., Sheffield, V, Weber, J.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          University, 6100 Main, Houst
Location/Qualifiers
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Direct Submission
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Strassmann, J.E., Hughes, C.R., Barefield, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   social wasps
social wasps
mol. Ecol. 5 (3), 459-461 (1996)
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Strassmann,J.E., Solis,C.R., Barefield,K. and Queller,D.C.
Trinucleotide microsatellite loci in a swarm-founding neotropical wasp, Parachartergus colobopterus and their usefulness in other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Parachartergus colobopterus.
Parachartergus colobopterus
Parachartergus colobopterus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Arthropoda;
Eukaryotae; mitochondrial eukaryotes; Hymenoptera; Apocrita;
Tracheata; Hexapoda; Insecta; Petrygota; Hymenoptera; Apocrita;
Aculeata; Vespoidea; Vespidae; Polistinae; Parachartergus.
                                                                                                                                                                                                                                                                                                                                                 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii;
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31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59
                                                                                                     jeff-murray@uiowa.edu
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complement(137..156)
164..208
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/clone="Paco3301CAT"
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denature:
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Pred. No.
0; Misma
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la; Theria; Eutheria; Archonta; Primate
30 seconds at 94 degrees
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3.44e-15;
--hes 0;
                                                                                                                                                     City, IA 52242, USA
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Query Match
Best Local S
Matches 3
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Best Local S
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGATGATGATGATGATGATGATGATGCC
                                                                                                                                                                                                                              Dib.C. Faure,S., Fizames,C., Samson,D., Drouot,N., Vignal,A., Millasseau,P., Marc,S., Hazam,J., Seboun,E., Lathrop,M., Gyapa, Morissette,J. and Weissenbach,J.

A comprehensive genetic map of the human genome based on 5,264
                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (01-SEP-1995) Genethon, B.P.
E-mail: Jean.Weissenbach@genethon.fr
                                                                                                                                                                                                                                                                                                                                                     Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo 1 (bases 1 to 298)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSB346YB5 298 bp DNA ST9
H.sapiens (D1S2781) DNA segment containing
AFMb346yb5; single read.
                                                                                                                                                                                                                                                                                                                                                                                                                         CA repeat; dinucleotide repeat; GT repeat; microsatellite DNA; microsatellite marker; repeat polymorphism; STS.
h 2.0%;
Similarity 97.0%;
32; Conservative
                                                                                                                                                                                           Nature 380 (6570), 96176476
                                                                                                                                                                                                                     microsatellites
                                                                                                                                                                                                                                                                                                                                            Weissenbach,J.
                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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Similarity 100.0%;
31; Conservative
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                                                                                                                                                                                                                                                                                        (bases 1 to 298
                                                                                                                                                                              automatic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(134..153)
37 c 62 g
                                                                  /clone_lib="genomic DNA"
/chromosome="1"
107 c 33 g 6
                                                                                                          /note="cloning vector is M13mp18"
/cell_line="CEPH 134702"
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                                                                                                                                    /organism="Homo sapiens"
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KCl:
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Total Vol:
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Pred. No. 3.44e-15;
0; Mismatches 0
Score 31; DB 203;
Pred. No. 3.44e-15;
0; Mismatches 1
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50mM
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8.3.
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each 1.5 pmole
each 200 uM
0.3 units
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                         Length 298;
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repeat; clone
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RESULT 9
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                                                  Query Match 2.0%;
Best Local Similarity 100.0%;
Matches 32; Conservative
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catcatcatcatcatcatcatcgtcatcacagc
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STS sequence; primer; sequence tagged site.
human vector-pJCP1 host-E.coli dut+ung+ (DH10B) Marker Selected genomic DNA prepared from XY individual of French nationality.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Catarrhini; Hominidae; Homo.

1 (bases 1 to 314)

Murray, J., Sheffield, V, Weber, J.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Primer A: AGTACTTGTAAGAGTGCCTGGC
Primer B: GAAAATTTTCTGGACTGGGA
STS size: 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The University of Iowa Department of Pediatrics, Iowa City, Tel: (319) 356-3508 Fax: (319) 356-3347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;
                                                                                                                                                                                                             Equivalent set:
GATA21C11 GATA21D12 GGAA11C11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synonyms: ATC6, CHLC.ATC6.#T9592
Contact: Dr. Jeffrey C. Murray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cooperative Human Linkage Center Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo Sapiens
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                                                                                                                72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              jeff-murray@uiowa.edu
                                                                                                                 დ
                                                                                                                                     /organism="Homo Sapiens"
54.158
54.75
                                                                                                                                                                                                     ATC6
                                                                                                             complement(139..158)
87 c 46 g
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annealing:
extension:
PCR cycles:
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KCl:
Tris:
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Total Vol:
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                                                              Score 32; DB 197;
Pred. No. 1.07e-16;
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                                                 Mismatches
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each 1.5 pmole
each 200 uM
0.3 units
10 ul
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GCT14A05
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GGAA3A07
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RESULT 11
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Best Local
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A. thaliana
Z25512
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g941102
STS sequence; primer; sequence tagged site.
STS sequence; primer; sequence tagged site.
human vector=pJCP1 host=E.coli dut+ung+ (DH10B) Marker Selected human vector=pJCP1 hos
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cooperative Human Linkage Center Unpublished (1995)
Synonyms: ATCZF09, CHLC.ATCZF09.T7508
Contact: Dr. Jeffrey C. Murray
                            g396648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The University of Iowa
Department of Pediatrics,
Tel: (319) 356-3508
Fax: (319) 356-3347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Catarrhini; Hominidae; Homo.

1 (bases 1 to 377)
Murray,J., Sheffield,V, Weber,J.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primate
expressed
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PCR Profile:
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Primer B: CTGACTCCAGAGCTCGTGTT
                                                                                                                                                                                                                                                                                                  h 2.0%;
Similarity 80.0%;
48; Conservative
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KCl: 50mM
Tris: 10mM
PH: 8.3.
Location/Qualifiers
1.377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          jeff-murray@uiowa.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
44..207
44..63
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1 90 c 90 g
sequence tag; partial cDNA sequence
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transcribed
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Total Vol:
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Pred. No. 3.44e-15;
0; Mismatches 11;
                                                                           sequence;
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each 1.5 pmole
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C 10 sec. 64 C 10 sec. 72 C 20 sec.
58 C 10 sec. 72 C 20 sec. Mg++: 1.00;
Gel: Acrylamide 7%, Formamide 32%, Urea 34%
                                                                                                                                                                                           Otah, Dept. of Human Genetics
2160 Eccles Institute of Human Genetics
Salt Lake City, UT 84112
e-mail: sts@corona.med.utah.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (10-AUG-1993) CNRS, GDR-1003 ACS, INRA, laboratoire Biologie Moleculaire, BP 27, 31326 Castanet-Tolosan cedex, Fra E-mail:gdr-svp@toulouse.inra.fr. On behalf of: CNRS URA 1178, Laboratoire de Biologie Moleculaire vegetale, B.P. 53X, 38041 Grenoble Cedex, France. E-mail:FQUIGLEY@grenet.fr 2 (bases 1 to 514)
                                                                                                                            Primer A: ATTCCCCTGCCTTGGCCTC
Primer B: GAAGAATGCTGCCATC
End to Label: Primer B
PCR Profile:
                                                                                                                                                                                                                                                                 Genetic and physical mapping of simple sequence sequence tagged sites from the human genome Unpublished (1994)
Submitted by: Utah Center for Human Genome Resea
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Gerken, S.C., Matsunami, N., Plaetke, R., Albertsen, H., Ballard, L., Melis, R., Lawrence, E., Moore, M., Holik, P.R., Carlson, M., Zhao, X., Robertson, M., Bradley, P., Elsner, T., Tingey, A., Lalouel, J.-M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCR primer; STS sequence; microsatellite DNA; microsatellite marker; sequence tagged site; trinucleotide repeat.
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Human STS UT7996.
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1 (bases 1 to 514)
Quigley and Mache, R.
Direct Submission
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/tissue_type="Flower buds of A.tl
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Submitted by: Utah Center for Human Genome Utah, Dept. of Human Genetics 2160 Eccles Institute of Human Genetics Salt Lake City, UT 84112 e-mail: sts@corona.med.utah.edu Primer A: ATTCCCCTGCCTTGCCCTC Primer B: GAAGAATGGTGCCATCCATG End to Label: Primer B
PCR Profile:
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Gerken,S.C., Matsunami,N., Plaetke,R., Albertsen,H., Ballard,L., Melis,R., Lawrence,E., Moore,M., Holik,P.R., Carlson,M., Zhao,X., Melis,R., Lawrence,E., Moore,M., Holik,P.R., Carlson,M., Zhao,X.,
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58 C 10 sec. 72 C 20 sec. Mg++: 1.00:
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Best Local S
Matches 3
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                                                                                                                                                                                                                                                                        STS
                                                                                                                                                                                                                                                                                                  source
                                                                                                           15
                            277 bp DNA
human STS CHLC.GCT16B04.P18276
G09999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   588 bp. DNA STS human STS CHLC.ATC5A05.P10592 clone ATC5A05.G09471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Catarrhin; Hominidae; Homo.

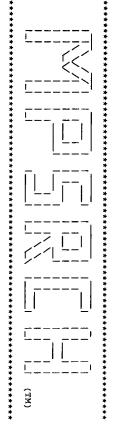
1 (bases 1 to 588)
Murray, J., Sheffield, V, Weber, J.L., Duyk, G. and Buetow, K.H.
Cooperative Human Linkage Center
Unpublished (1995)
Synonyms: ATCSA05, CHLC.ATC5A05.T10591
Contact: Dr. Jeffrey C. Murray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g941320
STS sequence; primer; sequence tagged site.
human vector-pJCP1 host-E.coli dut+ung+ (DH10B) Marker Selected
genomic DNA prepared from XY individual of French nationality.
9941848
STS sequence; primer; sequence tagged site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The University of Iowa Department of Pediatrics, Iowa City, IA 52242, USA Tel: (319) 356-3508 Fax: (319) 356-3347 Email: jeff-murray@uiowa.edu
                                                                                                                                                                                                                                                                                                                                                                                 Buffer:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protocol:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Primer A: AATGTCATCACCTTCTCTCCC
Primer B: TGTGGTGAGCTGAGATTGTG
STS size: 199
PCR Profile:
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Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;
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                                                                                                                                                              h 2.0%;
Similarity 100.0%;
31; Conservative
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                                                                                                                                                                                                                                                                                                          KC1: 50mM
Tris: 10mM
pH: 8.3.
Location/Qualifiers
                                                                                                                                                                                                                                                        /organism="Homo sapiens"
23..221
23..43
                                                                                                                                                                                                                              complement(202..221)
151 c 95 g
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extension:
PCR cycles:
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KCl:
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al Vol:
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Pred. No. 3.44e-15;
0; Mismatches 0;
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each 1.5 pmole
each 200 uM
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REFERENCE
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primer_bind
BASE COUNT
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            Search completed: Fri Apr 25 19:13:56 1997
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                                                                                                                  Query Match 1.9%;
Best Local Similarity 94.9%;
Matches 37; Conservative
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time: 1016 secs.
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                                                          45 GCCGCTGCTG-TGATGATGATGATGATGATGATGAT
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Primer B: TGTTGGATACAATTTAGGAAAGC
STS size: 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Department of Pediatrics, Iowa City, Tel: (319) 356-3508
Fax: (319) 356-3347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cooperative Human Linkage Center
Unpublished (1995)
Synonyms: GCT16804, CHLC.GCT16804.T18143
Contact: Dr. Jeffrey C. Murray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Catarrhini; Hominidae; Homo.

1 (bases 1 to 277)

Murray,J., Sheffield,V, Weber,J.L., Duyk,G. and Buetow,K.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;
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                                                                                                                                                                                                                         /organism="Homo sapiens" 6..147 6..25
                                                                                                                                                                                            complement(125..147)
1 50 c 63 g
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annealing:
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KCl:
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                                                                                                                  Score 30; DB 197;
Pred. No. 1.04e-13;
0; Mismatches 1
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degrees
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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Apr 25 12:04:26 1997; MasPar time 9.19 Seconds 583.635 Million cell updates/sec

Tabular output not generated.

Title: >US-08-699-716A-2
Description: (1-521) from US08699716A.pep
Perfect Score: 3546

Perfect Score: 3546
Sequence: 1 MGHHHHHHHHHHSSGHIDDD.....RFIQKYDSVMQRLLDDTSGK 521

Scoring table: PAM 150 Gap 11

1: 88003 seqs, 10295656 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-geneseq25

i:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18

Statistics: Mean 35.391; Variance 190.955; scale 0.185

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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16 102 2.9 17 99 2.8 18 100 2.8 19 100 2.8	102 2. 99 2. 100 2.	102 2. 99 2.	102 2.		103 2.	103 2.	105 3.	106 3.	106 3.	105 3.		106 3.	7 110 3.1	4	5 966 27.2	27		2 2233 63.0	1 2242 63.2	Result Query No. Score Match
793]		793	672	1529 1	663	257			708	493						151 1	170 1	329 1	329 1	Length I
LB W02283	L8 W02282	4 R20743	5 R31216	L8 R97985	3 R13139	7 R36675	_	14 R72826	2 R08402	3 R13992	10 R57771	17 R88503	L7 R96206	17 R95009	L4 R76527	L4 R76526	L4 R76528	L5 R79962	L5 R79961	DB ID
•	Murine receptor type	Murine receptor-type	Penicillin binding pr	CORK potassium channe	B.burgdorferi strain	30 kD Borrelia burgdo	Kinetochore protein C	Human mitosin.	AmIlO5 encoded by Ida	P. falciparum sporozo	Mouse nucleobindin.	Borrelia burgdorferi	Invasin protein.			tis	Yersinia pestis cafl	Partial LcrV (V antig	Partial LcrV (V antig	Description
3 830101	3.82e+01	3.82e+01	4.36e+01	2.92e+01	2.55e+01	2.55e+01	1.95e+01	1.70e+01	1.70e+01	1.95e+01	1.30e+01	1.70e+01	9.84e+00	3.06e-02	1.67e-63	1.17e-63	5.61e-74	1.80e-163	3.48e-164	Pred. No.

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	2.2
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1427	1338	1267	1098	1098	1069	953	953	936	926	926	924	924	652	423	414	350	303	302	183	183	183	183	3567
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R10534	R41731	R04232	R52747	R22103	R52748	R15159	R60072	R34547	R50291	R14482	R42385	R10889	R08403	R89408	R32020	R20230	R82096	R82097	R29943	R88704	R94724	R74640	R44431
Human 160kD mediator	High molecular weight	Rickettsia rickettsii	Bovine IL-2/LKT chime	Bovine IL-2 - LKT fus	Bovine IFNgamma/LKT c	Leukotoxin from P. ha		GnRH-leukotoxin gene	Recombinant leukotoxi	LKT352.	Recombinant leukotoxi	Leukotoxin 352 encode	AmW105 encoded by Was	tivat	Sequence of a eukaryo	hUOG-1.	Rat Gax protein.	Human Gax protein.	Deduced from Lelystad	Porcine reproductive	PRRSV Lelystad ORF-4	virus (eryA region polypepti
7.39e+01	6.48e+01		7.39e+01	5.68e+01	7.39e+01	7.39e+01	7.39e+01	7.39e+01	7.39e+01	7.39e+01		7.39e+01	7.39e+01		5.68e+01	6.48e+01	5.68e+01		6.48e+01		6.48e+01	6.48e+01	4.36e+01

ALIGNMENTS

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                                                                                                                                                                                                                        Query Match
Best Local S
Matches 32
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R79961-62 are encoded by T04222-23 (resp.), DNA sequences (lcrV) encoding R79961-62 are encoded by T04222-23 (resp.), DNA sequences (lcrV) encoding all or a protective epitopic part of the mature V protein of Yersinia pestis. The protein was expressed as a fusion protein with maltose binding protein or glutathione-S-transferase in 3 different plasmid vectors. v. pestis is the highly virulent causative organism of plague in a wide range of animals, including man. The V antigen (LcrV) is an unstable 37.3 kDa monomeric peptide encoded on the ca. 70 kb Lcr plasmid. The V antigen is postulated to act as a virulence antigen, and transformed microorganisms contg. recombinant DNA encoding a V antigen protein/peptide are useful in vaccines to protect against plague.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-APR-1996 (first entry)
Partial LcrV (V antigen) of Y. pestis.
LcrV; V antigen; virulence; plague; vaccine; epitope.
Yersinia pestis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MINA) UK SEC FOR Leary SEC, Titbal WPI; 95-328268/42.
                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant DNA expressing Yersinia pestis V antigen - useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; T04222
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08-MAR-1994; GB-004577
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14-SEP-1995.
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                   122 mavmhfsltadridddilkvivdsmnhhgdarsklreelaeltaelkiysvigaeinkhi 181
                                                                                                                                            314 MAVMHFSLTADRIDDDILKVIVDSMNHHGDARSKLREELAELTAELKIYSVIQAEINKHL 373
                                                                       254
                                                                       FANRVITDDIELLKKILAYFLPEDTILKGGHYDNQLQNGIKRVKEFLESSPNTQWELRAF 313
                                                                                          fanrvitddiellkkilayflpedailkgghydnglqngikrvkeflesspntqwelraf 121
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l Similarity 99.4%;
326; Conservative
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Pred. No. 3.48e-164;
1; Mismatches 0;
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RESULT RE
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Best Local S
Matches 32
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LcrV; V antigen; virulence; plague; vaccine; epitope.
Yersinia pestis.
W09524475-Al.
14-SEP-1995
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R79962;
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Leary SEC, Titball RW, Williamson
WPI; 95-328268/42.
N-PSDB; T04223.
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08-MAR-1994; GB-004577
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                                                                                                                             DNA constructs capable of transforming microorganisms used as live or attenuated vaccines which induce an in against Yersinia pestis, at mucosal surfaces. Disclosure; Page 16; 27pp; English. The sequence represents the Y. pestis cafl (F1) antigous from plasmid pFGAL2a. The DNA construct can be used the property of th
                                                                                                                                                                                                                                                                                                                                                                                                       (MINA) UK SEC FOR DEFENCE Howells A, Leary SEC, Oys WPI; 95-246396/32.
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Yersinia pestis cafl (F1) antigen.
Vaccine; antigen: Salmonella typhimurium;
bubonic plaque; pneumonic plaque.
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DNA constructs capable of transforming microorganisms - used as live or attenuated vaccines which induce an immu against versinia pestis, at mucosal surfaces.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence represents the Y. pestis caf1 (F1) antigen expressed from plasmid pFSIG3a. The DNA construct can be used to transform human or animal gut colonizing microorganisms, specifically attenuated Salmonella typhinurium or Salmonella typhinurium o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA constructs capable of transforming microorganisms used as live or attenuated vaccines which induce an imagainst Yersinia pestis, at mucosal surfaces. Disclosure, Page 18; 27pp; English. The sequence represents the Y. pestis cafl (F1) antige
                                                                                                                                                                                                                                                                                                                                                                                     which induce immune responses at mucosal surfaces. provide protection against infection with Y. pestis, parenterally and orally active vaccines offering pro-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MINA) UK SEC FOR DEFENCE. Howells A, Leary SEC, Oys WPI; 95-246396/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yersinia pestis caf1 (F1) antigen.
Vaccine; antigen; Salmonella typhimurium;
bubbnic plague; pneumonic plague.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        which induce immune responses at mucosal surfaces. The vacue provide protection against infection with Y. pestis, and are parenterally and orally active vaccines offering protection against bubonic and pneumonic plague.
                                                                                                                                                                                                                                                                                                                                               against bubonic and pneumonic plague. Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; Q92818.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-DEC-1994; G02818.
24-DEC-1993; GB-026425
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                                                                                                                                                                                                                                                                                                     Match
                                                                                                                                                                      svnftdaagdpmyltftsqdgnnhqfttkvigkdsrdfdispkvngenlvgddvvlatgs
                        dffvrsigskggklaagkytdavtvtvsnq 151
                                                                                                        vnftdaagdpmyltftsqdgnnhqfttkvigkdsrdfdispkvngenlvgddvvlatgsq 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SVNFTDAAGDPMYLTFTSQDGNNHQFTTKVIGKDSRDFDISPKVNGENLVGDDVVLATGS
  DFFVRSIGSKGGKLAAGKYTDAVTVTVSNQ
                                                                                    VNFTDAAGDPMYLTFTSQDGNNHQFTTKVIGKDSRDFDISPKVNGENLVGDDVVLATGSQ
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llarity 98.0%;
Conservative
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llarity 98.7%;
Conservative
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3; N
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                                                                                                                                                                                                                                                          re 966; DB 14;
1. No. 1.67e-63;
Mismatches 0;
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No. 1.17e-63;
    193
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Best Local
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23-OCT-1995; U13737.
24-OCT-1994; US-329154.
16-MAR-1995; US-405496.
14-APR-1995; US-422711.
07-JUN-1995; US-422711.
07-JUN-1995; US-480604.
(OPHI-) OPHIDIAN PHARM INC.
N-PSDB: 1.707.

Therapeutic delivery system utilibring very systemic bio-avariance not readily degraded in the gut, enhances systemic bio-avariance not readily degraded in the gut, enhances systemic bio-avariance of therapeutic agents

Example 1; Fig 1; 110pp; English.

The sequence represents a bacterial invasin protein, which may be complexed with a therapeutic agent to transport the agent across complexed with a therapeutic agent to transcytosis to increase
                                                                                                                                                                                                                                                                        20-OCT-1995; U13749.
27-OCT-1994; US-331393.
(AMGE) AMGEN INC.
Habberfield AD, Jensen-
WPI; 96-251447/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C. difficile type toxins, and to treat C. difficile intoxication, partic. diarrhoea
Claim 7; Page 340-342; 434pp; English.
pHlsBot fusion protein (R95009), the product of a nucleotide sequence (T29246) in vector pETHisa, comprises a polyhistidine affinity tag and fragment C (see also R95008) of the Clostridium botulinum type A neurotoxin. The pHisBot protein was expressed in Escherichia coli as a soluble protein and was purified by metal chelate affinity chromatography to obtain a product free of endotoxin contamination that may be useful as an immunogen in vaccine compsns.
Sequence 462 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein
/label=
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/label=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fusion proteins comprising non-toxin protein and part of toxin useful to form anti-toxins against Clostridium botulinum type A, C. difficile type toxins, and to treat C. difficile intoxication,
                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "C-terr
W09613250-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Invasin protein.
Invasin; drug delivery; gastrointestinal membrane; transcytosis; bioavailability; fusion protein; enterocyte; Peyers patch M-cell Yersinia enterocolitica strain 8081c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R96206
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N-PSDB; T29246.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W09612802-A1.
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                                                                                                                                                                                                                                                    N-PSDB; T27535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Region
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645.835
C-terminal receptor binding
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                                                                                                                                                                                                                                                                                                  Jensen-Pippo K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 150; DB 17;
Pred. No. 3.06e-02;
7; Mismatches 4
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                                                                                                             Claim 3; Page 46, Fig 2; 67pp; English.

Claim 3; Page 46, Fig 2; 67pp; English.

R88503 represents the Borrelia burgdorferi, exported plasmid protein A (EppA). EppA is a virulent protein of about 17 kD. EppA and its active fragments can be used to induce an immune response to pathogenic Borrelia burgdorferi (BB) in an animal. The sequence may be used to produce recombinant EppA expressed in E. coli. EppA is exported beyond the inner membrane and is present during the infectious, in vivo stages of virulent BB growth. Polynucleotides encoding EppA and anti-EppA antibodies can be used for the detection of pathogenic BB in a sample.
                                                                                                                                                                                                                                                                                                              17-JUN-1994; US-261825.
(REGC ) UNIV CALLFORNIA.
Blanco DR, Champion CI, Haake DA, Lovett MA, Miller JN;
WPI; 96-058208/06.
W-PSDB; T10931.
Borrelia burgdorferi exported plasmid protein A - used to develop prods, to induce an immune response to B.burgdorferi and as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bioavailability 5- to 100-fold. may be linked via a degradable |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9535114-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Borrelia burgdorferi.
Key Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      parenteral administration.
                                                                                                                                                                                                                                                                                              diagnostic markers for Lyme disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Borrelia burgdorferi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R88503 standard; Protein; 174 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide
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115 ikgypnsifdyliqldsdk-idyaekyge-karenfeesykkdkitavkqilkqilad 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lyme disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sig_peptide
21..174
                                Similarity 34.5%;
20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33
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                                                                                                        174 AA;
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                                Score 106;
Pred. No. 1.
12; Mismatc
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                                  Mismatches
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No. 9.84e+00;
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                       42;
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                                                                Length 174;
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    THE SECTION OF THE PROPERTY OF
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Nuc protein binds DNA and augments anti-DNA antibody prodn. The protein is from human or mouse tissue or cells, esp. lymphocytes. Anti-nuc protein antibodies may be used to treat diseases involving
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nuc protein; nucleobindin; antibody; augmenting factor; DNA binding; p55.
/note= "vector-encoded_peptide"
Ep-447956-A.
25-SEP-1991.
14-MAR-1991; 103920.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R57771;
21-SEP-1994
                                                                                                                                                                                                                                                                                  Key
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                                                                                                                                                                                                                                                                                                                                                                                                                     R13992 standard; Protein; 493
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(MITK ) MITSUI TOATSU CHEM
(YOSH-) YOSHIYUKI KANAI GH.

WPI: 94-077375/10.
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26-NOV-1990; JP-324888
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                                                                                                                    /note= "amino acids 1-462
Region 484..493
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l Similarity 19.8
36; Conservation
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larity 19.8%;
Conservative
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22..483
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1..21
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la; antibodies;
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57; M
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23-MAR-1990; CH-000970

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16-MAY-1991
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WPI; 91-282989/39.
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                                                                                                                                                                                                                                                                                                                                                                       standard; Protein;
"tandem"
                                                 "tandem"
                                                                    104..108 conserved sequence 127..155
                                                                                                                                                                                                      "tandem"
                                                                                                                                                                                                                                                       "tandem"
                   133..137 conserved sequence 156..183
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llarity 21.6%;
Conservative
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Pred. No. 1.95e+01;
19; Mismatches 38
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Matches 2
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Disclosure; Fig 12; 167pp; English.
Antigens raised to the repeated peptide epitop can be used to prepare vaccines against Anapla preferred are peptides from the following sequences aparentheses:

ADSSSASGQQQESSVSSQS-[EASTSS]-QIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "homologous to sew
W09012030-A.
18-OCT-1990; U01678.
30-MAR-1990.
06-APR-1989; US-335178.
                  Purified mammalian protein mitosin and agents that bind it and inhibit its action - used to promote cell growth or to inhibit cell division and/or proliferation Claim 4; Fig 8B; 61pp; English.

R72829 is human mitosin. Mitosin is involved in the regulation of the mammalian mitotic cell cycle. Mitosin as with E2F-1 (see R72824) interacts with the retinoblastoma protein (the retinoblastoma tumour suppressor gene product). Mitosin is first synthesised at the G1/S boundary, it is then phosphorylated from S through M phase, and during mitosis, is closely associated with the centromeres/kinetochores at the mitotic spindle poles. Mitosin is necessary for a eukaryotic cell to enter the M phase of the mitotic cell cycle and its degradation is necessary for a cell to advance on to the next stage. Mitosin is thus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Region
/label=
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R72826
                                                                                                                                                                                                                                                                                                                                                                                               24-OCT-1994; U12162.
22-OCT-1993; US-141239.
(TEXA ) UNIV TEXAS SYST
Lee W, Zhu X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cell cycle; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 See also R08401-R08405. Sequence 708 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 90-334801/44.
N-PSDB; Q07041.
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McGuire TC, Palmer GH, Barbet AF, Davis WC,
     useful
                                                                                                                                                                                                                                                                                                                                                 N-PSDB; Q86851.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9511309-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= internal_repeat
Region 1660..1839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              348 LREELAELTAELKIYSVIQAEINKHLSSSGTINIHDKSINLM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'label= internal_repeat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard;
for controlling cell growth as overexpression
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larity 21.6%;
Conservative
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30; M
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.70e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diagnosis -
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RESULT THE SUCCESSION OF SUCCE
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Best Local S
Matches 7
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Sequence 2482 AA;
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                       08-DEC-1995;
09-DEC-1994;
                                                                                              /note= "the C-terminal domain is p:
form a proline-rich (10.6%) highly
basic (pI 10) globular domain"
wo9617867-A1.
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Kinetochore protein; CENP-F;
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                                                                                                                                                                                                                                                                                                                                                   - Globular_domain
"globular domain consists
s of 95 amino_acids"
                                                                                                                                                                                                                                                                                                      1620..1750 Extended_coiled_structure
                                                                                                                                                                                                       C-terminal_domain
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; US-353700.
; US-353700.
CHASE CANCER CENT.
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ibody, antibody
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119; M
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L.70e+01;
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                                                                                                                                                                                                                                                                           30 kD Borrelia burgdorferi protein Virulent; Lyme disease; antigen. Borrelia burgdorferi B31. W0308286-A. 29-APR-1993; U09145. 21-CCT-1991; US-781355.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattner
WPI; 96-
N-PSDB;
                                                                                                                                                                                                     (TEXA )
Barbour
WPI; 93-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           by immunofluorescence microscopy only during the G2 and M phases of a cell cycle. It is the product of a cDNA clone (T34578) isolated from a breast carcinoma cDNA ilbrary. Recombinant CENP-can be produced by expression in prokaryotic or eukaryotic host cells. CENP-F can be used to detect autoimmune antibodies to the protein, which may provide an early diagnosis for the onset of various malignant diseases. Use of CENP-F as a cell cycle marker allows the specific detection of G2 and M phase cells.
Claim 6; Fig 5; 88pp; English.
The 30 kD protein was identified in low-passage virulent
B. burgdorferi, but was absent in isogenic high-passage a
strains. The 30 kD protein was partially sequenced and a
                                                                                             DNA segment encoding 30 kD Borrelia by polypeptide - used in diagnosis or proburgdorferi associated diseases, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R36675
R36675;
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A 372 kDa human kinetochore protein, CENP-F (R99795),
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21-DEC-1990; E02282.
22-DEC-1989; DE-942728.
23-DEC-1989; DE-942728.
13-JUN-1990; DE-01988.
13-JUN-1990; DE-01988.
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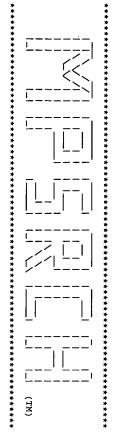
18-JUN-
                                                                                                                                                                                                                                                                                                                                                                  Protein p100 was isolated from a B.burgdorferi cell lysate and the N-terminal amino acid sequence was determined. A probe pool was synthesised and used to screen a B.burgdorferi cDNA library. A clone conty. the 5' 346 nucleotides of the p100 coding sequence was identified and sequenced. Cloning the entire gene allowed the p100 amino acid sequence to be deduced. See also 012744-012747, 013297-B and R13140-R13142.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            oligonucleotide probe was synthesised and used to identify DNA encoding the 30 kD protein in a low-passage virulent B. burgdorferi DNA library.
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WO9109870-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R13139;
27-SEP-1991 (first entry)
B.burgdorferi strain PKo p100 gene.
lyme borrellosis; vaccine; flagellin;
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R13139 standard; Protein;
   476
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Local Similarity 18.3%;
les 39; Conservative
NDLVSQKTTQLSDITSRFNSAIEALNRFIQKYDSVMQRLLDDTS 519
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                                                            eel-dkkaidldkaqqkldfaednld--iqr-dtvreklqenin
                                                                                                                      QTTIQVDGSEKKIVSIKDFLGSENKRTGALGNLKNSYSYNKDNNELSHFATTCSDKSRPL 475
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Similarity 18.3%;
19; Conservative
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                                                                                                                                                                                                                                               Score 103; DB 3; Length 663; Pred. No. 2.55e+01; 33; Mismatches 48; Indels
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Pred. No. 2.55e+01;
66; Mismatches 97; Indels 11;
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Search completed: Fri Job time : 56 secs.

Apr 25

12:05:22 1997

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Apr 25 12:02:44 1997; MasPar time 18.34 Seconds 809.706 Million cell updates/sec

Tabular output not generated.

Title: >US-08-699-716A-2 (1-521) from US08699716A.pep 3546

Description: Perfect Score: Sequence: 1 MGHHHHHHHHSSGHIDDD......RFIQKYDSVMQRLLDDTSGK 521

Scoring table: PAM 150 Gap 11

Searched: 89912 segs, 28507787 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

1:ann1 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3 8:unann4 9:unann5 10:unann6 11:unann7 12:unann8 13:unann9 14:unann10 15:unenc 16:unrev

Mean 51.015; Variance 156.464; scale 0.326

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1 2 3 3 3 4 3 4 3 1 1 1 1 1 1 1 1 1 1 1 1 1	Result
2245 2192 1108 168 168 127 127 123 123 123 123 123 123 123 123 123 123	Score
66 60 60 60 60 60 60 60 60 60 60 60 60 6	Query Match Length
326 326 170 168 1168 1168 1168 1168 1285 2076 220 220 333 411 2529 2529 2529 364 410 168 264 178 264 187 187 187 187 187 187 187 187 187 187	
9 9 8 9 9 8 1 1 1 1 1 1 1 1 1 1 1 1 1 1	DB ID
B3301 B37314 B37314 B37316 B37316 S07904 S07904 S34952 S47608 S447608 S448450 S	D
lorV protein - Yersi regulatory protein L capsular antigen F1 WT1 - human CS3 pilin precursor hypothetical protein CS3 finbrial protein CS3 finbrial protein actin homolog YJL081 median body protein fatty-acyl-coA synth hypothetical protein ribokinase (EC 2.7.1 Brn-3.2 - mouse transcription factor transcription factor transcription factor farscription factor protein bNA-directed RNA pol surface-located memb NIF1 protein - yeast gamma-giardin - Giar	Description
9.45e-274 1.08e-274 1.08e-124 4.08e-05 3.73e-01 8.48e-01 8.48e-01 8.48e-01 1.56e+00 1.56e+00 1.27e+00 1.27e+00 1.27e+00 2.32e+00 2.32e+00 2.32e+00 3.32e+00 4.19e+00 4.19e+00	Pred. No.

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120K surface-exposed	hypothetical protein	karyopherin beta – r	hypB protein – Alcal	kinesin-related prot	ATP-dependent protea	phosphoprotein phosp	nucleobindin precurs	hypothetical protein	cAMP receptor subtyp	١	hypBl protein - Alca	nucleoprotein N - to	exported protein - L	hypothetical protein	surface-array protei	outer cell wall prot	protein pl15 homolog	coatomer complex bet	invasin - Yersinia e	invasin - Yersinia e	hypothetical protein	DNA repair protein (епуеторе ргосети - в
1.93e+01	1.93e+01	2.33e+01			2.80e+01	1.60e+01	1.60e+01	1.93e+01	2.33e+01	2.33e+01	2.33e+01	2.33e+01	2.33e+01	1.10e+01	1.33e+01	9.08e+00	1.33e+01	9.08e+00	1.10e+01	1.10e+01	1.33e+01	1.10e+01	T.TUe+OI

ALIGNMENTS

!	Qy	DЬ	Qy Db	Оу	ОУ	Оу	3 H O	ORGA DATE ACCE REFE REFE REFE REFE	TIJ
	436	o 241 gsenkrtgalgnlknsysynkdnnelshfattcsdksrplndlvsgkttglsditsrfns 300	b 181 sgtinihdksinlmdknlygytdeeifkasaeykilekmpqttiqvdgsekkivsikdf1 240 	o 121 vmhfsltadridddvlKvivdsmnhhgdarsklreelaeltaelkiysviqaeinkhlss 180 	o 61 nrvitddiellkkilayflpedailkgghydnglgngikrvkeflesspntqwelrafma 120 	1 mirayeqnpqhfiedlekvrveqltghgssvleelvqlvkdknidisikydprkdsevfa 60 	Query Match 63.3%; Score 2245; DB 9; Length 326; Best Local Similarity 99.4%; Pred. No. 9.45e-282; Matches 324; Conservative 2; Mismatches 0; Indels 0; Gaps 0;	ORGANISM #formal_name Yersinia peštis DATE 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 23-Mar-1993 ACCESSIONS B33601 REFERENCE Price, S.B.; Leung, K.Y.; Barve, S.S.; Straley, S.C. #journal Molecular analysis of lcrGVH, the V antigen operon of #cross-references MUID:90008806 #accession B33601 ##status preliminary ##molecule_type DNA ##residues 1-326 ##label PRI ##cross-references GB:M5405 SUMMARY #length 326 #molecular-weight 37226 #checksum 6238	ENTRY B33601 #type complete TITLE lcrV protein - Yersinia pestis

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ACCESSIONS
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#authors
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#title
                        #authors Galyov, E.E.; Smirnov, O.Y.; Karlishev, A.V.; Vo
Denesyuk, A.I.; Nazimov, I.V.; Rubtsov, K.S.;
V.M.; Dalvadyanz, S.M.; Zav'yalov, V.P.
#journal FEBS Lett. (1990) 277:230-232
#title Nucleotide sequence of the Yersinia pestis gene antiqen and the primary structure of the prote T and B cell epitopes.
#cross-references MUID:9109503
#accession $13008
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 ##molecule_type
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##cross-references GB:M57893
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Similarity 96.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bergman, T.; Hakansson, S.; Forsberg, A.; Norl
Macellaro, A.; Backman, A.; Boelin, I.; Wol
J. Bacteriol. (1991) 173:1607-1616
Analysis of the V antigen lcrGVH-yopBD operon
                                                                                                                                                                                    $13008 #type complete capsular antigen F1 precursor - fromal_name Yersinia pestis 12-Feb-1993 #sequence_revision
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                                                                                                                                                                        18-Jun-1993
DNA
1-170 ##label
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Pred. No. 2.08e-274;
7; Mismatches 4;
  GAL
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                                                                gene encoding F1 protein. Putative
                                                                                                                                  Volkovoy, K.I.;
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##residues 1-16
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Similarity 100.0%;
170; Conservative
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#authors Jalajakumari, M.B.; Thomas, C.J.; Halter, R.; Manning, P.A.
#journal Mol. Microbiol. (1989) 3:1685-1695
Genes for biosynthesis and assembly of CS3 pili of CFA/II
enterotoxigenic Escherichia coll: novel regulation of pilus
production by bypassing an amber codon.
#cross-references_MUID:90158116
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##cross-references GB:S75264;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hamilton, T.B.; Barilla, K.C.; Romaniuk, Nucleic Acids Res. (1995) 23:277-284 High affinity binding sites for the Wilms
                                                                                                                                                                                                     S07904 #type complete
CS3 pilin precursor - Bscherichia coli
#formal name Escherichia coli
13-Jan-1995 #sequence_revision 13-Jan-1995
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#product capsular antigen Fl #status experimental #label
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Pred. No. 1.88e-124;
0; Mismatches 0;
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Pred. No. 4.08e-05;
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NID:g896246; CDS_PID:g896247
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NCE S66775
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##residues 1-1
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# #length 168 #molecular-weight 17491 #checksum
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                                                                                                                                                                                                                        / Match 3.6%;
Local Similarity 47.1%;
hes 16; Conservative
                                                                                                                                                                                                                                                                                                                                     ##experimental_source strain S288C
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Local Similarity 24.1%;
nes 41; Conservative
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                            A34952 #type complete
CS3 finbrial protein precursor - Escherichia coli
#formal_name Escherichia coli
07-Sep-1990 #sequence_revision 07-Sep-1990 #text_
04-Nov-1994
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#length 1116 #molecular-weight 125381 #checksum
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#formal_name Saccharomyces cerevisiae
28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change
02-Aug-1996
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S57374
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hypothetical protein YOL087c -
 A34952
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                                                                                                                                                                                                                      Score 127; DB 11;
Pred. No. 3.73e-01
7; Mismatches 1:
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                                               07-Sep-1990 #text_change
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##molecule_type_DNA
##residues 1-168 ##label
##cross-references GB:M35657
                                                           #submission
                                                                                                                                                                                                                                                                  #accession
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                                            #accession
                                                                                                                 #authors
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                                                                                                                                              ##cross-references EMBL:X83502
##note the nucleotide sequence was submitted
Library, December 1994
                                                                                                                                                                                                        ##molecule_type DNA
##residues 1-489 ##label MIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ##molecule_type DNA
##residues 1-489 ##label WIN
                       ##molecule_type
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Similarity 23.5%;
40; Conservative
                                                     S56855
Mlosga, T.; Schaaff-Gerstenschlaeger, I.; Baur, A.; Boles, E.; Chalwatzis, N.; Fournier, C.; Schmitt, S.; Velten, C. Wilhelm, N.; Witzel, A.; Zimmermann, F.K. submitted to the Protein Sequence Database, September 1995
                                                                                                                                                                                                                                                                           Sequence analysis of a 33.1 kb fragment from the left arm of Saccharomyces cerevisiae chromosome X, including putative proteins with leucine zippers, a fungal Zn(II)(2)-Cys(6) binuclear cluster domain and a putative alpha-2-SCB-alpha-2 binding site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    847608 #type complete
actin homolog YJL081c - yeast (Saccharomyce
protein J1012; protein YJL081c
#formal_name Saccharomyces cerevisiae
11-Nov-1994 #sequence_revision 11-Nov-1994
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Infect. Immun. (1988) 56:3297-3300
Nucleotide sequence of the gene encoding the major subunit
CS3 fimbriae of enterotoxigenic Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                          Miosga, T.; Schaaff-Gerstenschlaeger,
Baur, A.; Boles, E.; Fournier, C.; (
Wilhelm, N.; Zimmermann, F.K.
Yeast (1995) 11:681-689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #product (or 17-168) CS3 fimbrial protein #status
predicted #label MAT
#length 168 #molecular-weight 17464 #checksum 9103
                                            S56858
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DNA
1-489 ##label MIW
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Pred. No. 8.48e-01
48; Mismatches 7
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Best Local Similarity 25.8%;
Matches 16; Conservative
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##cross-references EMBL:X64517
## #length 857 #molecular-weight 100583 #checksum
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Local Similarity 20.1%;
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 Mol.
                                                                                                         #type complete
fatty-acyl-CoA synthase (EC 2.3.1.86) beta chain - yeast
(Yarrowia lipolytica)
#formal_name Yarrowia lipolytica, Candida lipolytica
30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
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J. Mol. Biol. (1993) 231:521-530
Sequence and structure of a new microtubule bundle in Giardia.
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#formal_name Giardia lamblia
06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
                                               Koettig, H.; Rottner, G.; Beck,
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Pred. No. 8.48e-01
21; Mismatches 2:
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                                               K.F.;
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Matches 34; Conservative
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Similarity 31.3%;
25; Conservation
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#length 220 #molecular-weight 24846 #checksum
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Thierry, A.; Fairhead,
Yeast (1990) 6:521-534
The complete sequence
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02-Dec-1994 #sequence_revision 02-Dec-1994 #text_change
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Pred. No. 1.56e+00;
39; Mismatches 69
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Pred. No. 8.48e-01;
22; Mismatches 28
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                            C.; Dujon,
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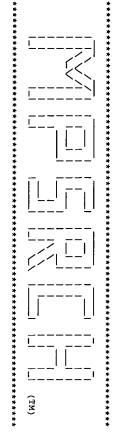
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##cross-references EMBL:X59720
                                                                                                                                                                                         174 hhhhhhhhhhhqphqalegellehlspglalgamagpdgtvvstpahaphmatmnpmhqa 233
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                                                                                                                                   234 alsmahahglp-shmgcmsdvdad 256
                                                                                                                                                                                                                                                                                                                                                      ##residues 1-411 ##label RES 1-415 ##cross-references GB:S68377; NID:g545068; CDS_PID:g545069
                                                                                                                                                                                                                                                                                                                                                                                       ##molecule_type mRNA
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                                                                                                                                                                                                                                                       Match 3.4%;
Local Similarity 28.6%;
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                                                     14
                                                                                                    RITLTYKEGAPITIMD-NGNIDTE
                                                                                                                                                                      HHHHHHHHHSSGHIDDDDKHMKKISSVIAI-ALFGTIATANAADLTASTTATATLVEPA
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Similarity 23.2%;
22; Conservative
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3R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S19445
A56923 #type complete transcription factor shn melanogaster)
                                                                                                                                                                                                                                                                                                     gene name Brn-3.2
#length 411 #molecular-weight 43172 #checksum
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Neuron (1994) 12:205-218
Brn-3-2: a Brn-3-related transcription factor with
distinctive central nervous system expression and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #formal_name Mus sp. #common_name mouse
26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change
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#length 333 #molec
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Pred. No. 1.27e+00;
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                    fruit fly (Drosophila
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ORGANISM
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NDS DNA binding; transcription factor; zinc finger
NDS #length 2529 #molecular-weight 271637 #checksum
                                                                                                                                                                                                                                                      ##molecule_type mRNA ##label ARO
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Local Similarity 24.6%;
hes 32; Conservation
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195 lptvdsnhii 204
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                                                                                                                                     80 ataaaaaaaaaatttvttaatptkkr-tyretatattvtqrstnkaniaaaialaaate 138
                                                                                                                                                                                             Match 3.4%;
Local Similarity 24.6%;
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                                   GTTSTSVNFTDAAGDPMYLTFTSQDGNNHQFTTKVIGKDSRDFDISPKVNGENLVGDDVV 157
                                                                                                                                                                                                                                                                                                                                                         Arora, K.; Dai, H.; Kazuko, S.G.; Jamal, J.; O'Connor, Letsou, A.; Warrior, R.
Cell (1995) 81:781-790
The Drosophila schnurri gene acts in the Dpp/TGFbeta signaling pathway and encodes a transcription factor homologous to the human MBP family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 melanogaster)
#formal_name Drosophila melanogaster
11-Aug-1995 #sequence_revision 11-Aug-1995
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11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change
25-May-1996
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                                                                                                                                                                                                                                                     #molecular-weight 277600 #checksum
                                                                                                                                                                          Score 119; DB 12;
Pred. No. 1.90e+00;
38; Mismatches 55
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Pred. No. 1.90e+00;
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Ω |:| :: 158 LATGSQDFFV 167

Search completed: Fri Apr 25 12:04:07 1997 Job time : 83 secs.

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Apr 25 12:01:35 1997; MasPar time 13.01 Seconds 849.481 Million cell updates/sec

Tabular output not generated.

Description:
Perfect Score:
Sequence: >US-08-699-716A-2 (1-521) from US08699716A.pep 3546

1 MGHHHHHHHHHSSGHIDDD......RFIQKYDSVMQRLLDDTSGK 521

Scoring table: PAM 150 Gap 11

Searched: 59021 seqs, 21210388 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

swiss-prot34
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11

Statistics: Mean 53.350; Variance 126.457; scale 0.422

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Result No.
2245 2192 2192 2192 2127 127 123 123 123 123 115 110 110 110 110 110 110 110 110 110	Score
63 311 31 31 31 31 31 31 31 31 31 31 31 3	Query Match
326 110 1168 489 8489 8489 8489 2076 333 813 973 1173 3111 1173 3111 1173 3111 1173 11	Length
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0.00e+00 0.00e+00 1.64e-160 3.28e-02 9.09e-02 9.09e-02 9.09e-02 9.09e-01 1.93e-01 1.93e-01 1.93e-01 1.93e-01 1.94e+00 2.14e+00 2.14e+00 2.14e+00 2.14e+00 2.14e+00 3.37e+00 5.37e+00 5.37e+00 5.37e+00	Pred. No.

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CYTOCHROME P450-TERP	CENP-F KINETOCHORE PR	MYOSIN HEAVY CHAIN A	CELLULOSE BINDING PRO	DNA REPAIR PROTEIN RA	HYPOTHETICAL 105.2 KD	DNA-BINDING PROTEIN R	LAMIN A.	CARBON CATABOLITE DER	DISCONNECTED PROTEIN.	FLAGELLIN 2.	PROBABLE METHIONINE A	MYOGLOBIN.	MAJOR ANTIGEN.	120 KD SURFACE-EXPOSE	IMPORTIN BETA SUBUNIT	AMINOPEPTIDASE II (EC	KINESIN-LIKE PROTEIN	CLPB PROTEIN.	HYPOTHETICAL 65.5 KD	PUTATIVE KINESIN-LIKE	SERINE/THREONINE PROT	MICOLN DEAVI CHAIN, C
1.63e+01	8.43e+00	1.05e+01	1.31e+01	8.43e+00	1.31e+01	8.43e+00	1.05e+01	1.31e+01	1.05e+01	1.05e+01	8.43e+00	1.31e+01	5.37e+00	5.37e+00	5.37e+00	6.74e+00	3.40e+00	6.74e+00	6.74e+00	4.28e+00	3.40e+00	4.200100

ALIGNMENTS

рb	DЪ	Qy Db	рb	Ma Ma	SER DRAG COCAL PAR ROCCOORDED DO
181 sgtinihdksinlmdknlygytdeeifkasaeykilekmpqttiqvdgsekkivsikdf1 240 	121 vmhfsltadridddvlkvivdsmnhhgdarsklreelaeltaelkiysviqaeinkhlss 180 	61 nrvitddiellkkilayflpedailkgghydnglqngikrvkeflesspntqwelrafma 120 	1 mirayeqnpqhfiedlekvrveqltghgssvleelvqlvkdknidisikydprkdsevfa 60 	Query Match 63.3%; Score 2245; DB 5; Length 326; Best Local Similarity 99.4%; Pred. No. 0.00e+00; Matches 324; Conservative 2; Mismatches 0; Indels 0; Gaps 0;	LCT 1 1 1CT_YERPE STANDARD; PRT; 326 AA. P21206; P21206; P21206; P21206; P1-MAY-1991 (REL. 18, CREATED) P1-MAY-1991 (REL. 18, CAST SEQUENCE UPDATE) P1-MAY-1993 (REL. 26, LAST SEQUENCE LOCUS PROTEIN P1-MAY-1993 (REL. 26, LAST SEQUENCE S.S., STRALEY S.C.; P1-MAY-1993 (REL. 18, LEUNG K.Y., BARVE S.S., STRALEY S.C.; P1-MACTERIOL. 171:5646-5653(1989). P1-MACTION: POSSIBLY INVOLVED IN CA(2+) REGULATION OF YOR EXPRESSION, WHICH INCLUDES THE EXPORT PROCESS. P1-MS-1-SUBCELLULAR LOCATION: SECRETED. EMBL; M26405; G155450; ALT_SEQ. P1R; B33601, B33601. PLASMID; ANTIGEN; VIRULENCE. P1-MS-1-SUBCELLULAR LOCATION: SECRETED. P1-MS-1-MS-1-MS-1-MS-1-MS-1-MS-1-MS-1-MS

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Best Loc
Matches
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BERGMAN T., HARANSSON S., FORSBERG A., NORLAND BAECKMAN A., BOELIN I., WOLF-WATZ H.;

J. BACTERIOL. 173:1607-1616(1991).

-:- FUNCTION: INVOLVED IN CA(2+) REGULATION OF INCLUDES THE EXPORT PROCESS.

-:- SUBCELLULAR LOCATION: SECRETED.

EMBL; M57893; G15448; -.

PIR; B37314; B37314.
CAF1_YERPE
P26948;
01-AUG-1992
01-AUG-1992
01-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YERSINIA
PLASMID P
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LCRV_YERPS
P23994;
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01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)
01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
VIRULENCE-ASSOCIATED V ANTIGEN (LOW CALCIUM R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PLASMID PIB1 PROKARYOTA;
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326 AA;
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   (REL.
(REL.
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larity 96.6%;
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                                                                            STANDARD;
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24,
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LAST SEQ
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 SEQUENCE UP
ANNOTATION
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Pred.
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No. 0.
                       UPDATE)
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Best I
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STRAIN-PB176;
STRAIN-PB176;
MEDITINE; 90158116.
JALAJAKUMARI M.B., THOMAS C.J., HAI
MICROBIOL. 3:1685-1695(1989).
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1583_ECOLI STANDARD;

P15488;
01-APR-1990 (REL 14, CR
01-APR-1990 (REL 14, LA
01-OCT-1996 (REL 34, LA
01-OCT-1996 (REL 34, LA
01-OCT-1996 (REL 34) (R
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FR
MEDLINE; 89
BOYLAN M.,
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MEDLINE; 91099503.

GALYOV E.E., SMIRNOV O.Y., KARLIS
DENESYUK A.I., NAZIMOV I.V., RUBS
DALVADYANZ S.M., ZAV'YALOV V.P.;
FEBS LETT. 277:230-232(1990).
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CHAIN
  EMBL;
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ESCHERICHIA COLI.
PROKARYOTA; GRACI
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PIR; S
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PLASMID PERA.
PROKARYOTA; GRACILICUTES;
ENTEROBACTERIACEAE.
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                                                                                                                                                               LEVINE M.M.;
                                                                                                                                                                                                                                              STRAIN-E9034A;
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BACTERIOL. 171:6372-6374(1989).

- FUNCTION: FIMBRIAE (ALSO CALLED PILI), POLAR FROM THE SUTFACE OF THE BACTERIUM TO A LEGIOMICROMETERS AND NUMBERING 100-300 PER CELL, COLONIZE THE EPITHELIUM OF SPECIFIC HOST OR IBL; X16944; G41161; -.
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L; X61996; G48621; -.
; S13008; S13008.
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170; Conser
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100
                                                                                                                                                                                                                                                                                                                         FROM N.A.
89032631.
., SMYTH C.J., SCOTT J.R.
IMMUN. 56:3297-3300(1988)
                                                                                                                                                                                      90036735.
                                                                                                                                                                                                                                                                    OF 23-45.
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larity 100.0%;
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, LAST SEQUENCE UPDATE)
, LAST ANNOTATION UPDATE
T A PRECURSOR (CS3 PILIN)
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                                                                                                                                                                                      JR.,
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F1 CAPSULE ANTIGEN.
CONTAINS POTENTIAL &
THAT MAY STIMULATE THAT MAY STATEM
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Pred. No. 1.64e-160;
0; Mismatches 0;
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PILIN).
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ABRAMOV V
                                                  POLAR FILAMENTS
LENGTH OF 0.5-1.
CELL, ENABLE BACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P.A.;
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                                                                                                                                                                                         .F.,
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                                                     BACTERIA
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                                                                                      RADIATING
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Best Local :
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Best Local
                                                                        Matches
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MEDLINE; 95024194.

MEDLINE; MARWAN &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ULT 5
ACT3 YEAST STANDARD
P80428;
01-FEB-1995 (REL. 31, C
01-FEB-1995 (REL. 31, L
01-NOV-1995 (REL. 32, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
SEQUENCE
                                                                                                                                                                           EMBL; Z49356; G1008244; -.
PIR; S47608; S47608.
LISTA; SC01441; ACT3.
SGD; L0000027; ACT3.
PROSITE; PS01132; ACTINS_ACT_LIKE.
                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                              MIOSGA T., SCHAAFF-GERS
BOLES E., FOURNIER C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HARATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACTIN-LIKE PROTEIN ACT3.
ACT3 OR YJL081C OR J1012.
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE; 94336725.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FIMBRIA;
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                                                                                                                                                 SEQUENCE
                                                                                                                                                                STRUCTURAL
                                                                                                                                                                                                                                                                                                                                                YEAST 11:681-689(1995)
                                                                                                                                                                                                                                                                                                                                                                   ZIMMERMANN F.K.
                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 96093911.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               141
   93
                                     22
                                                                                                                                                                                                                                                    CHAILARITY: TO ACTIN. STORM APPLIANTLY.

OF THE ARPA SUBFAMILY.

GBL; X75317; G436808; -.

GBL; X83502; G92875; -.

GBL; Z49356; G1008244; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            L; M35657; G145627; A34952; A34952; A34952.; S07904; S07904.
                      DISPKVNGENLVGDDVVLATGSQDFFVRSIGSKGGK-LAAGKYTDAVTVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MKKISSV-IAIALFGTIA-TANAADLTASTTATATLVEPARITLTYKEGAPITIMDNGNI
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, SIGNAL.
1
                                                                                         Similarity
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                                                                        16;
                                                                                                                                              PROTEIN;
489 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KARWAN
                                                                                                                                                                                                                                                                                                                                                                                SCHAAFF-GERSTENSCHLAEGER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACAD.
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larity 24.1%;
Conservative
                                                                     3.5%;
larity 25.8%;
Conservative
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168
83
17491
                                                                                                                                            CYTOSKELETON.
54831 MW; C41435B1 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WINTERSBERGER U.;
. U.S.A. 91:10757-10757(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WINTERSBERGER U.;
. U.S.A. 91:8258-8262(1994).
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                                                                                                                                                                                                                                                                                                                             STRONG,
                                                                     Score 123; DB 1; Lo
Pred. No. 9.09e-02;
21; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 127; DB 4; L
Pred. No. 3.28e-02;
47; Mismatches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    z
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Best Local
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STRAIN-PORTLAND-1;
MEDLINE, 93287123.
MARSHALL J., HOLBERTON D.V.;
J. MOL. BIOL. 231:531-530(1993).
-!- FUNCTION: MAY HAVE A ROLE IN IN
BETWEEN CELL DIVISIONS.
-!- SUBCELLULAR LOCATION: MEDIAN BET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LT 6
MEDB_GIALA
                                                                                                                                                                                                             p34229;
p34229;
p1-FeB-1994 (REL. 28, CREATED)
p1-FeB-1994 (REL. 28, LAST SEQUENCE UPDATE)
p1-FeB-1994 (REL. 28, LAST SEQUENCE UPDATE)
p1-FeB-1994 (REL. 28, LAST SEQUENCE UPDATE)
p1-FATTY ACID SYNTHASE, SUBUNIT BETA (EC 2.3.1.86) (CONTAINS: 3-FATTY ACID SYNTHASE, SUBUNIT BETA (EC 2.3.1.86) (CONTAINS: 3-FATTY ACID SYNTHASE (EC 4.2.1.61);
p1-FATTY ACID SYNTHASE (EC 1.3.1.9);
p1-FATTY ACID SYNTHASE THIOESTERASE (EC 2.3.1.38);
p1-FATTY ACID SYNTHASE THIOESTERASE (EC 3.1.2.14)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X64517; G312671; EMBL; X64517; G312671; CYTOSKELETON; MICROTUBULES; SEQUENCE 857 AA; 100583 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UP)
01-OCT-1996 (REL. 34, LAST ANNOTATION |
MEDIAN BODY PROTEIN.
GIARDIA LAMBLIA (GIARDIA INTESTINALIS)
EUKARYOTA; PROTOZOA; SARCOMASTIGOPHORA
                 SEQUENCE FROM N.A.
STRAIN=CX 161-1 B ADEL
MEDLINE; 91238709.
KOETTIG H., ROTTNER G.,
                                                                                                                                            EUKARYOTA;
                                                                                                                                                                     YARROWIA LIPOLYTICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FAS1_
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SSSGTINIHDKSINLMDKNLYG-YTD-EEIFKAS
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TIG H., ROTTNER G., BECK K.-F., GEN. GENET. 226:310-314(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           _YARLI
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                                                                                                                                            FUNGI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.5%;
larity 20.1%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32, CREATED)
32, LAST SEQUENCE UPDATE)
34, LAST ANNOTATION UPDAT
                                                                                                                                         CA (CANDIDA LIPOLYTICA)
ASCOMYCOTINA; HEMIASCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AN ALPHA-HELICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SARCOMASTIGOPHORA; MASTIGOPHORA; DIPLOMONADIDA;
                                                                   A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COILED COIL; HEPTAD MW; 5E2BBA84 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 124; DB 6;
Pred. No. 7.06e-02;
71; Mismatches 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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FRESULTION OF THE STATE OF THE 
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Best Local S
Matches 2
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01-FEB-1995 (REL. 3
01-FEB-1995 (REL. 3
HYPOTHETICAL 24.8 K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LONG-CHAIN FATTY ACIDS FROM ACETYL-COA, MALONYL-COA AND NADPH.

THE BETA SUBUNIT CONTAINS DOMAINS FOR: [ACYL-CARRIER PROTEIN]

ACETYL-TRANSEERASE AND MALONYL-TRANSEERASE, S-ACYL FATTY ACID

SYNTHASE THIOESTERASE, ENOYL-[ACYL-CARRIER PROTEIN] REDUCTASE, AND

SYNTHASE THIOESTERASE, ENOYL-[ACYL-CARRIER PROTEIN] REDUCTASE, AND

SYNTHASE THIOESTERASE, ENOYL-[ACYL-CARRIER PROTEIN] DEBYDRAFASE.

-I-CARRIYTIC ACTIVITY: ACETYL-COA + NALONYL-COA + 2N NADPH =

LONG-CHAIN FATTY ACID + (N+1) COA + N CO(2) + 2N NADPH =

LONG-CHAIN FATTY ACID + (N+1) COA + N NALONYL-COA + 2N NADPH =

LONG-CHAIN FATTY ACID + (N+1) COA + N CO(2) + 2N NADPH =

CATALYTIC ACTIVITY: ACETYL-COA + [ACYL-CARRIER PROTEIN] = COA

+ ACETYL-[ACYL-CARRIER PROTEIN].

-I-CATALYTIC ACTIVITY: MALONYL-COA + [ACYL-CARRIER PROTEIN] = COA

+ MALONYL-[ACYL-CARRIER PROTEIN].

-I-CATALYTIC ACTIVITY: (3R)-3-HYDROXYPALMITOYL-[ACYL-CARRIER PROTEIN]

-I-CATALYTIC ACTIVITY: (3R)-3-HYDROXYPALMITOYL-[ACYL-CARRIER PROTEIN]
                                                                       STRAIN-S288C / AB972;
BARRELL B.G., BADCOCK K., BANKIER A.T., BOWMAN S., BROWN D.,
CHURCHER C.M., CONNOR R., COPSEY T., DEAR S., DEVLIN K., FRASER
GENTLES S., HAMLYN N., HORSNELL T.S., HUNT S., JAGELS K., JONES
LOUIS E., LYE G., MOULE S., MOULE T., ODELL C., PEARSON D.,
RAJANDREAM M.A., RILES L., ROWLEY N., SKELTON J., SMITH V.,
WALSH S.V., WHITEHEAD S.;
SUBMITTED (DEC-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; Z38113; G558397; -.
EMBL; Z4816, C4047; G763339; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YIA7_YEAST P40555;
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ACT_SITE
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                             SACCHAROMYCES
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                           HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                    EUKARYOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
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CATALYTIC ACTIVITY: OLEOYL-[ACYL-CARRIER PROTEIN] +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           = 2-HEXADECENOYL-[ACYL-CARRIER PROTEIN] + H(2)O.
CATALYTIC ACTIVITY: ACYL-[ACYL-CARRIER PROTEIN] + NAD(+) = 2,3-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT: FATTY ACID SYNTHETASE ARE [ALPHA(6)BETA(6)]
TWO MULTIFUNCTIONAL SUBUNITS (ALPHA & BETA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACYL-CARRIER PROTEIN + OLEATE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TSQDGNNHQFTTKV-IGKDSRDFDISPKVNGENLVGDDVVLATGSQDFFVRSIGSKGGKL 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S48450; S48450
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Similarity 31.3%;
25; Conservation
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SE; HYDROLASE; LI
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1156 1647
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276 276
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2076 AA; 23022
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31, LAST SEQUENCE UPDATE)
31, LAST ANNOTATION UPDATE)
KD PROTEIN IN FAA3-BET1 INTERGENIC
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LIGASE; NAD; NADP.
ACETYL TRANSFERASE.
ENOYL REDUCTASE.
DEHYDRATASE.
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Pred. No. 9.
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ACETYL TRANSFERASE (BY SIMILARITY).
MALONYLTRANSFERASE (BY SIMILARITY).
MM; E10A5234 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
  B3911075 CRC32
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1.09e-02;
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Best Local
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Best Local Similarity 22.8%;
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
SEQUENCE;
                                                                                                                                             NIP1_YEAST STANDARD; PRT; 812 AA. P32497; 91-0CT-1993 (REL. 27, CREATED) 01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE) 01-0CT-1996 (REL. 34, LAST ANNOTATION UPDATE) NUCLEAR TRANSPORT PROTEIN NIP1. NIP1 OR YM3309C OR YM9924 (DC OR YM9952.11C. SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGD;
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EMBL; X59720; E264378; -.
PIR; S12918; KIBYRB.
LISTA; SC00940; RBK1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RBK1 OR YCR36W OR YCR523.
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)
                                                                                                                      EUKARYOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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01-MAY-1992 (REL. 22, LAST SEQ
01-FEB-1994 (REL. 28, LAST ANN
PROBABLE RIBOKINASE (EC 2.7.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RBSK_YEAST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00583; PFKB_KINASES_1.
PROSITE; PS00584; PFKB_KINASES_2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ST 6:521-534(1990).

CATALYTIC ACTIVITY: ATP + D-RIBOSE = ADP + D-RIBOSE 5-PHOSPHATE.

PATHWAY: FIRST STEP IN RIBOSE METABOLISM.

SIMILARITY: BELONGS TO A FAMILY OF CARBOHYDRATE KINASES THAT

GROUPS TOGETHERS PEKB, FRUK, GSK, LACC, RBSK, AND SCRK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qgetlsmaikfstlassltiqrkgaaesmplykdv 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   klmnrkkrgivvmtlgsrgvlfcshespevqflpaiqnvsvvdttgagdtflgglvtqly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         L0001587; RBK1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KDKNIDISIKYDPRKDSEVFANRVITDDIELLKKI 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KLAAGKYTDAVTVTVSNQEFMIRAYEQNPQHFIEDLEKVRVEQLTGHGSSVLEELV-QLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hllqrshvllnqhfdnmnvksnqdarrn-nddqaiqytipfafisevvpgspsdkadikv 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YFLPEDTILKGGHYDNQLQNGIKRVKEFLESSPNTQWELR-AFMAVMHFSLTADRIDDDI 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.48;
Similarity 23.28;
22; Conservation
   FROM N.A.
93066237.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91181345
                                                                                                                  FUNGI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNGI;
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                                                                                                                      ASCOMYCOTINA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ASCOMYCOTINA; HEMIASCOMYCETES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36984 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
EC 2.7.1.15).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 120; DB 8;
Pred. No. 1.93e-01
25; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3E1772EC CRC32;
                                                                                                                  HEMIASCOMYCETES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120; DB 11;
No. 1.93e-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       182
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                                                                                                                                                                                                                                                                   UPDATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 333;
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Best Local S
Matches 3
                                                                                                                                               J. BIOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                            COPB_YEAST STANDARD; PRT; 973 AA. P41810; PRT; 975 AA. 01-NOV-1995 (REL. 32, CREATED) O1-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE) O1-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-S288C / AB972;
CHURCHER C.M., LOUIS E.J., BARRELL B.G., I
SUBMITTED (NOV-1995) TO EMBL/GENBANK/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONNOR R., CHURCHER C.M., BARRELL B.G., RAJANDREAM M
SUBMITTED (APR-1995) TO EMBL/GENBANK/DDBJ DATA BANKS
-!- FUNCTION: INVOLVED IN TRANSPORT OF PROTEINS TO THE
PROBABLY VIA ITS SERINE-RICH ACIDIC N-TERMINAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LISTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; L02899; -; NOT_ANNOTATED_CDS.
EMBL; Z54141; G984682; -.
EMBL; Z49212; G798951; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <u>.</u>
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                                                                                                                                                                      DUDEN
                                                                                                                                                                                              STRAIN-RSY255
                                                                                                                                                                                                        SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                 EUKARYOTA;
                                                                                                                                                                                                                                             SACCHAROMYCES CEREVISIAE (BAKER'S
                                                                                                                                                                                                                                                                    COATOMER BETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 571-812 FROM N.A.
                                                                                                                                                                                MEDLINE; 95014199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSPORT;
                                                                                                                                                                                                                                                                                                                                                                               366
                                                                                                                                                                                                                                                                                                                                                                                                      757
                                                                                                                                                                                                                                                                                                                                                                                                                              308
                                                                                                                                                                                                                                                                                                                                                                                                                                                      700
                                                                                                  BIOL. CREM. 269:24486-24495(1994).

BIOL. CREM. 269:24486-24495(1994).

FUNCTION: THE COATOMER IS A CYTOSOLIC PROTEIN COMPLEX THAT REVERSIBLY ASSOCIARIES WITH GOLGI MEMBRANES TO FORM VESICLES MEDIATE BIOSYNTHETIC PROTEIN TRANSPORT FROM THE ER, VIA THE UP TO THE TRANS GOLGI NETWORK. THE COATOMER COMPLEX TO FOR BUNDING EPOM CONCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBURIT: MONOMER. SUBCELLULAR LOCATION: CYTOPLASMIC;
                      FOR BUDDING FROM GOLGI MEMBRANES.
SUBUNIT: OLIGOMERIC COMPLEX THAT CONSISTS OF AT LEAST THE ALPHA,
BETA, BETA, (ADMA, DELTA, EPSILON AND ZETA SUBUNITS.
SUBCELLULAR LOCATION: PERIPHERAL MEMBRANE PROTEIN ASSOCIATED WIT
NON-CLATHRIN COATED VESICLES AND CISTERNAE OF THE GOLGI COMPLEX,
BUT EXISTS ALSO AS A SOLUBLE CYTOSOLIC COMPLEX. THE EQUILIBRIUM
BETWEEN THOSE TWO FORMS MAY BE REGULATED BY GTP, ATP, OR BETA-CO
 PHOSPHORYLATION (BY SIMILARITY). PTM: THE N-TERMINAL IS BLOCKED.
                                                                                                                                                                                                                                                                                                                                                                              QAEINKHLSSSGTINIHDKSINLMDK-NLYGYTDEEIFKASAEYKI
                                                                                                                                                                                                                                                                                                                                                                                                                                          wallpnmetvlnslt-ervqveslktyffsfkrfyssfsvakl-aelfdl-penkvvevl
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                                                                                                                                                                                                                                                                                                                                                                                                      qsvia-eleipakln-dektifvvekgdeitkleeamvklnkeyki
                                                                                                                                                                                                                                                                                                                                                                                                                              WELRAFMAVMHFSLTADRIDDDILKVIVDSMNH-HGD-ARSKLREELAELTAELKIYSVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L0001252; NIP1
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NATL. ACAD. SCI. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 31; Conser
                                                                                                                                                                                                                                 FUNGI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROTEIN
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larity 29.2%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSPORT
                                                                                                                                                                                                         AND
                                                                                                                                                                                                                                                                  (BETA-COAT PROTEIN) (BETA-COP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           U.S.A.
                                                                                                                                                                                                         PARTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SHERMAN F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 115; DB 6;
Pred. No. 6.54e-01;
28; Mismatches 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SER-RICH.
V -> D (I
Q -> H (I
K -> N (I
K -> N (I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ASP/GLU-RICH (ACIDIC).
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89:10355-10359(1992)
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-> N (IN
47993DCE
                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                 HEMIASCOMYCETES
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REF. 1).
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CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
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                                                                                                                     VESICLES
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                                                                                                                                                                      SCHEKMAN
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                          OR BETA-COP
                                                                                                           REQUIRED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                      THAT
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Best Local S
Matches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 2
                                                                                                                                                                              GIAG_GIALA
P38413;
01-OCT-1994
01-OCT-1994
01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q99074;
01-JUN-1994 (REL.
01-JUN-1994 (REL.
01-JUN-1994 (REL.
                                                                                       GIARDIA LAMBLIA (GIARDIA INTESTINALIS). EUKARYOTA; PROTOZOA; SARCOMASTIGOPHORA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HA34_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSPORT; PROTEIN TRANSPORT; SEQUENCE 973 AA; 109033 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: SIGNIFICANT, THOSE OF BETA-ADAPTINS. EMBL; U11236; G595413; -. LISTA; SC01433; SEC26. SGD; L0001847; SEC26.
                                                                                                                                                          GIARDIN GAMMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X16984; G2488; -.
SPORULATION; STRUCTURAL PROTEIN.
SEQUENCE 173 AA; 16478 MW; 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 92033077.
JUDELSON H.S., MICHELMORE R.W.;
JUDELSON H.S., MICHELMORE R.W.;
MOL. PLANT MICROBE INTERACT. 3:225-2
PART MICROBE INTERACT. 3:225-2
PART MICROBE INTERACT. 3:225-2
PART MICROBIAN STRUCTURAL
INFECTION PROCESS OF B.LACTUCAE.
PART MICROBIAN STRUCTURE GERMINATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BREMIA LACTUCAE (LETTUCE DOWNY MILDEW).
EUKARYOTA; FUNGI; MASTIGOMYCOTINA; OOMYCETES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HAM34
   SEQUENCE
                                                                HEXAMITIDAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=REGEL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HAM34 PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RVEQLTGHGSSVLEEL-VQLVKDKNI-DISIKYDPRKDS-EVFANRVITDDIELLKKILA 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             riqdinannvgaleeltldilrvlnaedldvrskaldismdlatsrnaedvvqllkkelq 366
                                                                                                                                                                                                                                                                                                                                                                                                                                   LLVGTLTLGGYKTGTTSTSVNFTDAAGDPMYLTFTSQDGNNHQFTTKVIGKDSRD
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   FROM
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4 (REL. 30, LAST 9
6 (REL. 34, LAST )
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larity 20.3%;
Conservative
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; TISSUE=SPORE;
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N.A.,
                                                                                                                                                                                                                                                                                                               STANDARD;
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29,
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   AND
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LAST SEQUENCE UE
LAST ANNOTATION
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   SEQUENCE
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Pred.
53; M
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Pred.
28; M
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                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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   OF 145-156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 109; DB 4;
No. 2.70e+00
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No. 1.34e+00
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                                                                                             MASTIGOPHORA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 173;
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Best Local S
Matches
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PIR; S25163; S25163.
PIR; A48453; A48453.
CYTOSKELETON; MICROTUBULES.
311 AA; 35632 MW
                         RECN OR HI0070.
HAEMOPHILUS INF
PROKARYOTA; GRA
                                                                                                           FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F.
KERLAVAGE A.R., BULT C.J., TOMB J.F., DOUGHERTY B.A., MERRICK J.M.
MCKENNEY K., SUTTON G., FITZHUGH W., FIELDS C.A., GOCAYNE J.D.,
SCOTT J.D., SHIRLEY R., LIU L.-I., GLODEK A., KELLEY J.M.,
WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLOM E., COTTON M.D.,
UTTERBACK T.R., HANNA M.C., NGUYEN D.T., SAUDEK D.M., BRANDON R.C.,
FINE L.D., FRITCHMAN J.L., FUHRMANN J.L., GEOGHAGEN N.S.M.,
GNEHM C.L., MCDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,
VENTER J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOHRIA A., ALONSO R.A., PEATTIE D.A.;

MOL. BIOCHEM. PARASITOL. 56:27-37(1992).

-!- FUNCTION: GIARDINS ARE INVOLVED IN PARASITE ATTACHMENT TO THE INTESTINAL MUCOSA AND IN THE CYTOSKELETAL DISASSEMBLY AND REASSEMBLY THAT MARKS THE TRANSITION FROM INFECTIOUS TROPHOZOITE TO TRANSMISSIBLE CYST. THEY MAY INTERACT WITH OTHER CYTOSKELETAL PROTEINS SUCH AS MICROTUBULES IN THE MICRORIBBONS OR CROSSBRIDGES, TO MAINTAIN THE INTEGRITY OF THE VENTRAL DISC.

-!- SUBCELLULAR LOCATION: MICRORIBBONS OF VENTRAL DISC.

-!- SUBCELLULAR LOCATION: MICRORIBBONS OF VENTRAL DISC.

-!- DOMAIN: PREDICTED TO HAVE AN ABUNDANCE OF ALPHA-HELICAL STRUCTURES (86%). IT IS NOT EXPECTED TO HAVE THE HEPTAD REPEAT FOUND IN THE COLLED COIL OF ALPHA-TYPE FIBROUS PROTEINS.
                                                                                                                                                                                                                                                                                                                                                         01-NOV-1995 (REL.
01-NOV-1995 (REL.
01-OCT-1996 (REL.
              EMBL; U3269
DNA REPAIR;
                                                                                                                                                                                                                                                STRAIN-RD
                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-PORTLAND-1;
MEDLINE; 93116803.
                                                                                                                                                                                                                                   MEDLINE;
                                                                                                                                                                                                                                                                                        PASTEURELLACEAE
                                                                                                                                                                                                                                                                                                                                             DNA REPAIR PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                   P44496;
                                                                                                                                                                                                                                                                                                                                                                                                              RECN_HAEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      naslrplide-vfs-megrlkafdaenadfvgktkgykstfr-sevhsriraggskldal 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VMHFSLTADRIDDDILKVIVDSMNHHGDARSKLRE-ELAELTAEL-KIYSVIQAEINKHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 19.2%; 37; Conservative
                                                                                                                                                                                                                                  95350630.
                                                                                                                                                                                                                                                                                                    GRACILICUTES;
 ATP-BINDING.
29 36
                                                                                                                                                                                                                                                                                                                  INFLUENZAE
                                                                                                                                                                                                                                                           N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                          32,
34,
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                                                                                                                                                                                                                                                                                                                                          LAST SEQUENCE UPL
LAST ANNOTATION U
CN (RECOMBINATION
                                                                                                                                                                                                                                                                                                                                                                                   CREATED)
                                                     TO OTHER
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                                                                                                                                                                                                                                                                                                    SCOTOBACTERIA;
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67; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; L45838; G1007082; -. EMBL; U32799; G926270; -.
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LAST SEQUENCE UPDATE)

LAST ANNOTATION UPDATE)

FERASE (EC 2.3.1.8) (PHO
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Pred. No. 2.1
61; Mismatch
                                                                                                                                                                                                                                                    Score 109; DB 8; Le
Pred. No. 2.70e+00;
45; Mismatches 54;
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Search completed: Fri Apr 25 12:02:27 1997 Job time : 52 secs.

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25:BCT1 26:BCT2 27:BCT3 28:BCT4 29:BCT5 30:BCT6 31:BCT7 25:BCT1 26:BCT2 37:BCT3 28:BCT4 29:BCT5 30:BCT6 31:BCT7 32:BCT8 33:BCT9 34:GEN1 35:GEN2 36:HTG 37:INV1 38:INV2 39:LNV3 40:INV4 41:INV5 42:INV6 43:INV7 44:LNV8 45:INV9 46:NAM1 47:NAM2 48:NAM3 49:VRT1 50:VRT2 51:VRT3 52:PAT1 53:PAT2 54:PAT3 55:PAT4 56:PHG 57:PLN1 58:PLN2 59:PLN3 60:PLN4 61:PLN5 62:PLN6 63:PLN7 64:PLN8 65:PLN9 66:PLN1 67:PLN1 58:PLN9 65:PLN1 58:PLN7 64:PLN8 65:PLN9 65:PLN1 58:PLN1 59:PR11 70:PR11 71:PR15 72:PR16 73:PR17 74:PR18 75:PR19 76:PR11 70:PR11 77:PR11 71:PR15 72:PR16 73:PR17 74:PR18 75:PR19 76:PR11 77:PR11 71:PR15 72:PR16 73:PR17 74:PR18 75:PR19 76:PR11 77:PR11 71:PR11 71:PR15 72:PR16 73:PR17 74:PR18 75:PR19 76:PR11 70:PR11 77:PR11 71:PR11 71:PR1
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Listing first 45 summaries
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101:BCT 102:GEN 103:INV1 104:INV2 105:MAM 106:VRT
107:PHG 108:PLN 109:PRI1 110:PRI2 111:ROD 112:SYN
113:UNA 114:VRL
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ALIGNMENTS

inia pestis"	/organism="Yersinia pestis" /strain="KIM5"
	source 12100
iers	FEATURES Location/Qualifiers
	07-AUG-1989.
e,s.	kindly submitted by Price,S.
Computer readable copy of sequence [J. Bacteriol. (1989) In press]	COMMENT Computer readable copy o
	MEDLINE 90008806
5653 (1989)	JOURNAL J. Bacteriol. 171, 5646-5653 (1989)
	pestis
Molecular analysis of lcrGVH, the V antigen operon of Yersinia	TITLE Molecular analysis of lc
Price, S.B., Leung, K.Y., Barve, S.S. and Straley, S.C.	AUTHORS Price, S.B., Leung, K.Y.,
	REFERENCE 1 (bases 1 to 2100)
	Yersinia.
Eubacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;	Eubacteria; Proteobacter
	ORGANISM Yersinia pestis
	SOURCE 75kb virulence plasmid.
LcrG protein; LcrH protein; LcrV protein; V antigen.	KEYWORDS LcrG protein; LcrH prote
	NID g155448
	ACCESSION M26405
pestis lcrG, lcrV, and lcrH genes, compelete cds.	DEFINITION Yersinia pestis lcrG, lc
DNA BCT 27-MAR-1992	LOCUS YEPLCR 2100 bp
	RESULT 1

Result No.

Score

Query Match Length DB

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Pred. No

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Submitted (22-MAR-1996) A. Roggenkamp, Hygiene and Microbiology, University of Wuerzburg, Josef-Schneider Strasse 2, 97080
                                                                                                                                                                                                                                                                                                                                                                       Yersinia pseudotuberculosis.
Yersinia pseudotuberculosis
Eubacteria; Proteobacteria;
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Analysis of the V antigen lcrGVH-yopBD Operon of Yersinia pseudotuberculosis: Evidence for a regulatory role of Lcri
J. Bacteriol. 173, 1607-1616 (1991)
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Disikydprkosevpanrvitgdiellkkilayflpedailkgehydhqlqqgikrke
Eflessphydwelrapmaviipsltadriddbilkvivdsmuhhfdbarsklreelakt
Taelkiysvlqaeinkhlssggtinihdksinlwgydbeeifkasaeyktlek
MPQTTIQEGETEKKIVSIKNFLESEKKRTGALGNLKDSYSYNKDNNELSHFATTCSDK
SRPLNDLYSQKTTQLSDITSRFNSAIEALNRFIQKYDSVMQRLLDDTSGK"
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MKIFAGRSAEEIKPAERELLDEIKRQKERQPQHPYDGKRPRKFTMMRGQII"
553..1533
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/product="V-antigen"
/db_xref="PID:g155459"
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/product="V-antigen"
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/product="V-antigen"
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264..551
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241..246
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219..224
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Direct Submission
Submitted (22-MAR-1996) A
University of Wuerzburg,
Wuerzburg, FRG
                                                                                                                                                                                                                                                                                                                                                                                                                                               936;
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Yersinia enterocolitica
Eubacteria; Proteobacter
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Similarity 96.6%;
936; Conservative
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/db_xref="PID:e239988"
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/strain="Y-96-P"
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Josef-Schneider Strasse 2,
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University of Wuerzburg,
Wuerzburg, FRG
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Contribution of V antigen and anti-V antigen
infection with different Yersinia strains
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173 c 190 g 271 t
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               gtaatgcatttctctttaaccgccgatcgtatcgatgatgatattttgaaagtgattgtt
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Contribution of V antigen and anti-V antigen infection with different Yersinia strains
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Yersinia enterocolitica
Eubacteria; Proteobacteria;
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/db_xref="PID:e239987"
/db_xref="PID:g1405827"
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Submitted (22-MAR-1996) A
University of Wuerzburg,
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Yersinia enterocolitica (type 0:8)
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TAELKIYSVIQAEINKYLSNSGTINIHDKSINLMDKNLYGYTDEEIFKASÄEYKILEK
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University of Wuerzburg,
Wuerzburg, FRG
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/product="V antigen"
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/transl_table=11
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DISIKYDPKKDSEVFAERVITDDIELLKKILAYFLPEDAILKGEHYDNQLQNGIKRVK
EFLESSPNTQMELRAFMAVMHFSLTADRIDDDILLKVIVSMNHHGDARSKLREELAR
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/strain="WA-314"
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University of Wuerzburg,
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MPQTTIKDDELHEVGVIAGAEKQIVSIKNFLESENKRFGALGNIKDSYSYNDNELS
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/db_xref="PID:e239983"
/db_xref="PID:g1405833"
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/strain="NCTC"
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1 (bases 1) to 5383)
Galyov, E.E., Karlishev, A.V., Chernovskaya, T.V., Dolgikh, D.A., Smirnov, O.Yu., Volkovoy, K.I., Abramov, V.M. and Zav 'yalov, V.P. Expression of the envelope antigen F1 of Yersinia pestis is mediated by the product of cating gene having homology with the chaperone protein PapD of Escherichia coli FEBS Lett. 286 (1-2), 79-82 (1991)
                                                                                                                                                                                                                                                                                       Concern 'Biopreparation', 142380 Lyubuchany, revised by [5]
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Galyov,E.E., Smirnov,O.Yu., Karlishev,A.V.,
Denesyuk,A.I., Nazimov,I.V., Rubtsov,K.S., I
Dalvadyanz,S.M. and Zav'yalov,V.P.
                                                                                                                                                                      5 (bases 1 to 5383)
Karlyshev,A.V., Galyov,E.E.,
Abramov,V.M. and Zav'yalov,V
                                                                                                                                                                                                                                                   4 (bases 1 to 5383)
Karlyshev, A.V., Galy
CaflR gene and its r
                                                                                                                                                                                                                                                                                                                                                                                                                Nucleofide sequence of the Yersinia pestis gene encoding {\tt F1} antigen and the primary structure of the protein. Putative {\tt T} and {\tt B} cell
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Yersinia pestis
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                                                                 /organism="Yersinia
complement(1..906)
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            /codon_start=1
/db_xref="PID:g48623"
                                                    /gene="caflR"
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Moscow Region, Ussr
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4796 cagaattacttgttggtacgcttactcttggcggctataaaacaggaaccactagcacat 4855
                                                                                               tcactcttacatataaggaaggcgctccaattacaattatggacaatggaaacatcgata 4795
                                                               TCACTCTTACATATAAGGAAGGCGCTCCAATTACAATTATGGACAATGGAAACATCGATA
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ALGIGANLGDFGAISTDVTQADSQKNKQKKESGQRWRYRYNKYLQGGTSLNIASEEYA
TEGFIKKLADTLNTYCKENTRNDCREDYAKFKNKVQFMLSQSIPGSGTLNFSGYRKWY
RDSRSTTSFSVGYNHFFRNGMSLTLNLSKTQNINKYGEKTSELLSNIWLSFPLSRWLG
NNSINSNYQMTSDSHGNTTHEYGVYGEAFDRQLYWDYRERFNEKGRKYTSNALNLNYR
GTYGELSGNYSYDQTQSQLGIGVNGNMVITQYGITAGQKTGDTIALVQAPDISGASVG
YWDGMKTDFRGYTNYGYLTPYREYKVEINDYTLDNDAEITNNIVSVIPFKGAVVLAKF
NARIGGRLFLHLKRSDNKPUPFGSIYTIEGQSSSGIVGDNSGVYLTGLPKKSKILVK
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/translation="MLKQMTVNSIIQYIEENLESKFINIDCLVLYSGFSRRYLQISFK
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QYRMIPFWSFKGLLGRREINCEYLQPRICYLKERNIIGQCFNFRDLVFYSGIDSKCRL
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AERGLNTIKSRLTLGETYSDSSIFDSIPIKGIKIASDESMVPYYQWNFAPVVRGIART
QARVEVLRDGYTVSNELVPSGPFELANLPLGGGSGELKVIIHESDGTKQVFTVPYDTP
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NDTYDQYVHHMYNIYYNSLPIYNLNKRDGYDVEVIKRRNDNTIDCHYFLPIYCDDMEF
YNEMQVYHNNIVKPEMSVTLGLPKS"
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KEGAPITIMDNGNIDTELLVGTLTLGGYKTGTTSTSVNFTDAAGDPMYLTFTSQDGNN
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NQGLQLPGNYFVNVFVNGRKVDSGNIDFRLEKHNGKELLWPCLSSLQLTKYGIDIDKY
PDLIKSGTEQCVDLLAIPHSDVQFYFNQQKLSLIVPPQALLPRFDGIMPMQLWDDGIP
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IYPLDAAGVMVSVKNTQDYPVLIQSRIYDENKESEDPFVVTPPLFRLDAKQQNSLR
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IKLLVRPNELKGTPIQFAEKLSWKVDGGKLIAENPSPFYMNIGELTFGGKSIPSHYIP
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/db_xref="PID:g1072424"
/db_xref="SWISS-PROT:P26926"
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/db_xref="PID:g48621"
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/function="chaperone-like
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                                                                     catctgtctagtggtggcaccataaatatccatgataaatcaaattaacctcatggataaa
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The difference in the lcrv sequences between Y. pestis and Y. pseudotuberculosis and its application for characterization of pseudotuberculosis strains
pseudotuberculosis strains
Microb, Pathog. 12 (3), 165-175 (1992)
                                                                                                             226;
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llarity 94.2%;
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Pred. No. 2.42e-154;
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WT1=Wilms'
                       Brown, M.A., Jones, K.A., Nicolai, H., Bonjardim, M., McFarlane, R., de Jong, P., Quirk, J.P., Lehrach, H. & Physical mapping, cloning, and identification of containing BRCA1 proc. Natl. Acad. Sci. U.S.A. 92 (10), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-4366 (19), 4362-436
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Location/Qualifiers
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/db_xref="pID:9896247"
/db_xref="pID:9896247"
/translation="mGHHHHHHHHHHSSGHIEGRHMRRVPGVAPTLVRSASETSEKRP
/translation="mGHHMHHHHHHHHHSSGHIEGRHMRRVPGVAPTLVRSASETSEKRP
FMCAYPGCNKKFYFKLSHLQMHSRKHTGEKPYSCDFKDCERRFFRSDQLKRHQRRHTGV
KPFQCKTCQRKFSRSDHLKTHTRTHTGEKPFSCRWPSCQKKFARSDELVRHHNMHQRN
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryotae; mitochondrial eukaryotes; Viridiplantae; Charophyta/Embryophyta group; Embryophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Oryza.
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Brown, M.A.
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